

RESULT 3
888571
-Protein-C05B5-5-[imported]—Caenorhabditis-elegans
C;Species: Caenorhabditis elegans
C;Accession: EB8571
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A;Reference number: A75000; MRID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/sc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/
A;Accession: EB8571
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-885 <END>
A;Cross-references: GB:chr_III; PID:CAA83593.1; PID:93873993; GSPDB:GN00021; CESP:C05B5-5
A;Genetics:
A;Gene: C05B5.5
A;Map position: 3

RESULT 4
164215
Query Match 29.0%; Score 60; DB 2; Length 585;
Best Local Similarity 46.8%; Pred. No. 5.3;
Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
OY 7 LTGWIWLVWSVILVGASHDNQYKPEQ 34
Db 465 LSSTIQIVSULVGLGVSSQQDQNQBLQ 492

RESULT 4
164215
hypothetical protein MG144 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Accession: I64215
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 07-Dec-1999
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M., Fuhmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.C.;
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of *Mycoplasma genitalium*.
A;Reference number: A64200; MRID:96026346; PMID:7569993
A;Accession: I64215
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-279 <TIGR>
A;Cross-references: GB:039694; GB:I43967; MDR:91045822; PID:91045827; TIGR:MG144
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3

RESULT 5
A55542
Query Match 27.5%; Score 57; DB 2; Length 279;
Best Local Similarity 36.1%; Pred. No. 6.5;
Matches 13; Conservative 8; Mismatches 7; Indels 8; Gaps 1;
OY 2 NRLIELTGWLVWSVILVGSA-----SHIDNY 29
Db 231 SRSIINVFIWLVLIINVLLVSCLMIAAYAHLDGY 265

RESULT 5
A55542
sensor kinase regB - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Accession: A55542
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
R;Mosley, C.S.; Suzuki, J.Y.; Bauer, C.E.
J;Bacteriol. 176, 7566-7573, 1994
A;Title: Identification and molecular genetic characterization of a sensor kinase respo
sis.

A; Reference number: A55542; NUID: 95095926; PMID: 88002581
 A; Accession: A55542
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-441 <MOS>
 A; cross-references-->DB-T35379
 C; Genetics:
 C; Keywords: regB
 Query Match 27.5%; Score 57; DB 2; length 441;
 Best Local Similarity 40.9%; Pred. No. 10; Mismatches 8; Indels 0; Gaps 0;
 Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 4 LIELTGIVLWVSVLGVASH 25
 DB 146 MIEFGSWSVAVIVIGVIFLGAYAH 167

RESULT 6
 T11105
 H+-transporting two-sector ATPase (EC 3.6.3.14) protein B - side-necked turtle mitochondrial
 C; Species: mitochondrial Pelomedusa surufa
 C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
 C; Accession: T11105
 R; Gardo, R.; Meyer, A.
 Proc. Natl. Acad. Sci. U.S.A. 95, 14226-14231, 1998
 A; Title: Complete mitochondrial genome suggests diapsid affinities of turtles.
 A; Reference number: Z17248; NUID: 99045666; PMID: 9826682
 A; Accession: T11105
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-55 <ZAR>
 A; Cross references: EMBL:AF039066; NID:93599976; PID:93599981; PIDN:AD05054.1
 C; Genetics:
 C; Species: mitochondrial
 C; Superfamily: H+-transporting ATP synthase protein 8
 C; Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion
 Query Match 26.8%; Score 55.5; DB 2; Length 55;
 Best Local Similarity 37.0%; Pred. No. 2.1; Mismatches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;
 QY 5 IELTGIVLWVSVLGVASHIDWQP 31
 DB 12 IFITSWLILII-ILPKKNSHPNNSP 37

RESULT 7
 S62564
 hypothetical protein SPAC30D11.06c - fission yeast (*Schizosaccharomyces pombe*)
 C; Species: Schizosaccharomyces pombe
 C; Date: 16-May-1995 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C; Accession: T38593; S62564
 R; Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, November 1995
 A; Reference number: 221801
 A; Accession: T38593
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-426 <PPE2>
 A; Cross References: EMBL:267661; NID:91065887; PIDN:CAA91892.1; PID:91065893; GSPDB
 A; Experimental source: strain 972b; cosmid c30D11
 C; Genetics:
 C; Gene: SPAC30D11.06c
 A; Map position: 1L
 A; Introns: 46/2; 75/3

Query Match 26.8%; Score 55.5; DB 2; Length 426;
 Best Local Similarity 28.9%; Pred. No. 15; Mismatches 16; Indels 1; Gaps 1;
 Matches 11; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 2 NRNLTELTGIVLWVSVI-LIGVASHIDNNQPPPEASAV 38

QY	11	IVLVWSVILGVASHIDNYPP	32	proc. Natl. Acad. Sci. U.S.A. 99, 443-449, 2002 A;Title: The genome sequence of the facultative intracellular pathogen <i>Bacillus melitensis</i>
Db	2058	MVLAVAFTLGRRTIDRGQPP	2079	A;Reference number: AD3252; PMID:11756688 A;Accession: AGC489 A;Status: preliminary
RESULT 13				
A10225				A;Residues: 1-344 <KUR> A;Cross-references: GB:AEO08917; PIDN:AAL53082.1; PID:917983945; GSPDB:GN00175
				A;Experimental source: strain 16M A;Genetics: BME11901
				A;Map position: I C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase c C;Keywords: copier; electron transfer; membrane-associated complex; oxidoreductase;
				C;Gene: BME11901
				A;Title: Genome sequence of <i>Yersinia pestis</i> , the causative agent of plague.
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;Li, M.; Rutherford, K.; Simmonds, M.; Shelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: A10225 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-65 <KUR> A;Cross-references: GB:AL590842; PIDN:CA090669.1; PID:915979874; GSPDB:GN00175 A;Genetics: C;Gene: YPO1822				
QY				
Db				
RESULT 14				Search completed: February 6, 2003, 21:39:34 Job time : 21 secs
A90057				A90057 sortase [imported] - <i>Staphylococcus aureus</i> (strain N315) C;Species: <i>Staphylococcus aureus</i> C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: A90057 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiota, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of methicillin-resistant <i>Staphylococcus aureus</i> . A;Reference number: A89758; MUID:21311952; PMID:1418146 A;Accession: A90057 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-206 <KUR> A;Cross references: GB:BA000018; PID:913702478; PIDN:BAB43619.1; GSPDB:GN00149 A;Experimental source: strain N315 C;genetics: A;Gene: srtA
QY				
Db				
RESULT 15				AG3489 Query Match 25.8% Score 53.5; DB 2; Length 206; Best Local Similarity 42.9%; Pred. No. 14; Matches 12; Conservative 5; Mismatches 10; Indels 1; Gaps 1; C;Species: <i>Bacillus melitensis</i> C;Accession: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 22-Mar-2002 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, R.
QY				
Db				

OY 8 TGIVW--LIVSVILL-----GVASHIDNYQQPEQ 34
 ID :|||: 111: |||:|||:|||:|||:
 DB 238 SGWILTTVLVSLVMVLLWICCAVATAVEQYVPEK 273

RESULT 4
 Y144_MYCGE STANDARD; PRT; 279 AA.
 ID Y144_MYCGE
 AC P47390;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical protein MG144.
 GN MG144.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=96056346; PubMed=7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Kelley J.M., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G.,
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
 RA Mycugen D.T., Utterback T.R., Sauder M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu C., Lucier T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RA "The minimal gene complement of Mycoplasma genitalium.";
 RA Science 270:397-403(1995).
 RN [2]
 RP SEQUENCE OF 64-140 FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=94075230; PubMed=8253680;
 RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
 RT "A survey of the Mycoplasma genitalium genome by using random sequencing.";
 J. Bacteriol. 175:7918-7930(1993).
 --> 11. SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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 CC EMBL; AF03906; ADD0504.1; -.
 DR InterPro; IPR001421; AtmaseB_mit.
 DR Pfam; PF00895; ATP-synt_8; 1.
 KW Hydride ion transport; CF(0); Mitochondrion; Transmembrane.
 FT TRANSMEM 4 24 POTENTIAL.
 SO SEQUENCE 55 AA: 6536 MW; D8D4BC8F8651A001 CRC64;

Query Match 26.8%; Score 55.5; DB 1; Length 55;
 Best Local Similarity 37.0%; Pred No. 1.4;
 Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;
 RT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C30B01.06c in chromosome I.
 ID YAJ6_SCHPO
 AC 009906;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 OY 5 IELTMWIVLVSVILLGVASHIDNYOP 31
 DB i2 IFITSWLILL-IILPKRKHIPNNSP 37

RESULT 6
 YAJ6_SCHPO STANDARD; PRT; 426 AA.
 ID YAJ6_SCHPO
 AC 009906;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C30B01.06c in chromosome I.
 SPAC20B11.06c.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Schizosaccharomycotales; Schizosaccharomycetaceae;
 SC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Redlandteam M.A., Lyne M., Lyne R., Stewart A.,
 RA Sqouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor A., Davis P., Feltwell T., Fraser A.,
 RA Gemmells S., Gobbo A., Hamlin N., Harris D., Hidalgo J., Hodgetts G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Wolckert G., Kert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Query Match 27.5%; Score 57; DB 1; Length 279;
 Best Local Similarity 36.1%; Pred. No. 4.4;
 Matches 13; Conservative 8; Mismatches 7; Indels 8; Gaps 1;

QY 2 NLIELTGWIVLVSVILLGVASHIDNY 29
 DB 231 SRSIRHFWIIVLINVLLVSCLMIAAYAHLDGY 266

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CC

DR EMBL; IPR0008585; PROSITE; PS000701; SDH_CYT.

DR Pfam; PF01127; SdHCyt; 1.

DR PROSITE; PS01000; SDH_CYT_1; FALSE_NEG.

DR PROSITE; PS01001; SDH_CYT_2; 1.

KW Tricarboxylic acid cycle; Electron transport; Heme; Transmembrane;

KW Inner membrane; Complete proteome.

FT TRANSMEM 35 55 POTENTIAL.

FT TRANSMEM 68 88 POTENTIAL.

FT TRANSMEM 104 124 POTENTIAL.

FT BINDING 33 33 HEME (POTENTIAL).

FT BINDING 83 83 HEME (BY SIMILARITY).

SQ SEQUENCE 124 AA; 14341 MW; 58G6A046IAFCBIA CRC64;

Query Match 25.1%; Score 52; DB 1; Length 124; Best Local Similarity 52.9%; Pred. No. 8.5; Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLLIEGTGWIVVLLVVAVL 19

Db 102 KLVNITGWCWVGSVLL 118

RESULT 11

OCTC_BOVIN STANDARD; PRT; 612 AA.

ID O19094; AC 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Peroxisomal carnitine octanoyltransferase (EC 2.3.1.-) (COT).

CRT OR COT.

OS Bos taurus (Bovine).

OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

OX NCBI_TAXID=9913;

[1] SEQUENCE FROM N.A., AND MUTAGENESIS.

RT TISSUE=Liver;

RX MEDLINE=97433288; PubMed=9288928;

RA Cronin C.N.;

RT "cDNA cloning, recombinant expression, and site-directed mutagenesis of bovine liver carnitine octanoyltransferase -- Arg505 binds the carboxylate group of carnitine." Eur. J. Biochem. 247:1029-1037(1997).

-!- FUNCTION: BETA-OXIDATION OF FATTY ACIDS. THE HIGHEST ACTIVITY CONCERN THE C6 TO C10 CHAIN LENGTH SUBSTRATE.

CC -!- PATHWAY: Fatty acid beta-oxidation cycle.

CC -!- SUBUNIT: MONOMER (PROBABLE).

CC -!- SUBCELLULAR LOCATION: Peroxisomal (Potential).

CC -!- SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACYLTRANSFERASE FAMILY.

CC

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CC

CC EMBL; U65745; AAC48758; 1.

CC InterPro; IPR000542; Carn_acyltransf.

CC InterPro; IPR000865; Microbodies_C.

DR Pfam; PF00755; Carn_acyltransf; 1.

DR PROSITE; PS00439; ACYLTRANSF_C_1; 1.

DR PROSITE; PS00440; ACYLTRANSF_C_2; 1.

DR PROSITE; PS00342; MICROBODIES_CTER; FALSE_NEG.

DR transfierase; Acyltransferase; Fatty acid metabolism; Transport; Peroxosome.

KW ACT_SITE 327 327 POTENTIAL.

FT BINDING 505 505 INVOLVED IN SUBSTRATE (CARNITINE)

DR PROSITE; PS000701; SDH_CYT.

DR Pfam; PF01127; SdHCyt; 1.

DR PROSITE; PS01000; SDH_CYT_1; FALSE_NEG.

DR PROSITE; PS01001; SDH_CYT_2; 1.

KW Tricarboxylic acid cycle; Electron transport; Heme; Transmembrane;

KW Inner membrane; Complete proteome.

FT TRANSMEM 534 537 POLY-GLY.

FT SITE 610 612 MICROBODY TARGETING SIGNAL (POTENTIAL).

FT MUTAGEN 505 505 R->N: INCREASE OF KW TOWARDS CARNITINE.

FT SEQUENCE 612 AA; 70263 MW; 2D5D91A54CF8E2BA CRC64;

Query Match 25.1%; Score 52; DB 1; Length 612; Best Local Similarity 42.1%; Pred. No. 40; Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 GVASHIDNYQPQPPQSASVQ 39

Db 105 GRASHIETIYWPPKEGTQLE 123

RESULT 12

OX2_ACBAC STANDARD; PRT; 307 AA.

ID QX02_ACBAC

AC P50653;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1999 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome A1 subunit 2) (Oxidase BA(3) subunit 2).

GN CYAB.

OS Acetobacter aceti.

OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;

OC Acetobacter.

OX NCBI_TAXID=435;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=1023;

RX MEDLINE=93322308; PubMed=8392509;

RA Futaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H., Kawamura Y., Horinouchi S., Beppu T.;

RA "Characterization of a cytochrome a1 that functions as a ubiquinol oxidase in Acetobacter aceti".

RT J. Bacteriol. 175:4307-4314(1993).

CC -!- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.

CC -!- SUBUNIT: HETEROFERMER OF THE SUBUNITS 1, 2, 3 AND 4.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: SOME TO MITOCHONDRIAL OR BACTERIAL COX SUBUNITS.

CC -!- BUT LACK HEME-BINDING DOMAIN.

CC

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CC

CC EMBL; D13185; BAA02480; 1.

CC DR HSP; P18400; ICYN.

CC DR InterPro; IPR001505; Copper_Cua.

CC DR Pfam; PF00116; COX2; 1.

CC DR PRODOM; PD000131; COPPER_CUA; 1.

CC DR PROSITE; PS00013; PROKR_LIPOPORPROTEIN; 1.

CC KW Oxidoreductase; Transmembrane; Respiratory chain; Signal; Lipoprotein.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 307 UBQUINOL OXIDASE POLYPEPTIDE II.

FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).

FT TRANSMEM 46 66 POTENTIAL.

FT SEQUENCE 307 AA; 33921 MW; E66734B84410996D CRC64;

Query Match 24.9%; Score 51.5%; DB 1; Length 307;
 Best Local Similarity 32.5%; Pred. No. 24; Mismatches 13; Conservative 8; Indels 14; Gaps 5; Matches 1; Gap 1;

Qy 5 IELTGHN----IVLVWSVILGVASHIDNYQPPEOSASVQ 39
Db 87 IELTWGVPSPUILLFLAVITYQTCHSLDPVPKPLEANTK 126

RESULT 13

TCR_STRAG STANDARD: PRT; 458 AA.

ID TCR_STRAG ID P13924; DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Tetracycline resistance protein.
 GN TET.
 OS Streptococcus agalactiae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus
 OR NCBI_TaxID=1311;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90016790; PubMed=2677995;
 RA van der Leijle D.; Bron S.; Venema G.; Oskam L.; flanking open reading frames of plasmids pB10, pB913 and pAV158";
 RT Nucleic Acids Res. 17:7283-7294 (1989).
 CC -I- FUNCTION: RESISTANCE TO TETRACYCLINE BY AN ACTIVE TETRACYCLINE EFFLUX. THIS IS AN ENERGY-DEPENDENT PROCESS THAT DECREASES THE ACCUMULATION OF THE ANTIBIOTIC IN WHOLE CELLS. THIS PROTEIN FUNCTIONS AS A METAL-TETRACYCLINE/H⁺ ANTIPORTER.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLASE FAMILY).

CC -----
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CC -----
 DR EMBL; X15659; CAA33712.1; -
 DR PIR; C25599; YNSCG.
 DR InterPro; IPR001411; TCR-TetB.
 DR PRINTS; PRO1036; TCRRETB.
 KW Antibiotic resistance; transmembrane; transport; Symport; Plasmid.

FT TRANSMEM 12 33 POTENTIAL.
 FT TRANSMEM 81 100 POTENTIAL.
 FT TRANSMEM 111 129 POTENTIAL.
 FT TRANSMEM 140 162 POTENTIAL.
 FT TRANSMEM 165 185 POTENTIAL.
 FT TRANSMEM 201 221 POTENTIAL.
 FT TRANSMEM 223 240 POTENTIAL.
 FT TRANSMEM 256 276 POTENTIAL.
 FT TRANSMEM 297 317 POTENTIAL.
 FT TRANSMEM 324 344 POTENTIAL.
 FT TRANSMEM 346 365 POTENTIAL.
 FT TRANSMEM 432 451 POTENTIAL.

RESULT 14

YHV2_LACHE STANDARD: PRT; 104 AA.

ID YHV2_LACHE ID P22295; DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 11.8 kDa protein in HIV 5' region precursor (ORF2).
 OS Lactobacillus helveticus.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OR NCBI_TaxID=1587;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=481;
 RX MEDLINE=9103544; PubMed=2228964;
 RA Joerger M.C.; Klaenhammer T.R.;
 RT "Cloning, expression, and nucleotide sequence of the Lactobacillus helveticus 481 gene encoding the bacteriocin helveticin J.";
 RL J. Bacteriol. 172:6339-6347(1990);
 CC -----
 CC EMBL; M53360; AAA6273.1; -
 DR PIR; B37145; B37145.
 KW Hypothetical Protein; Signal.

FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 104 HIPOHETICAL 11.8 KDA PROTEIN.

SO SEQUENCE 104 AA; 11809 MW; 39981885462D4C9B CRC64;

Query Match 24.4%; Score 50.5%; DB 1; Length 104;
 Best Local Similarity 47.8%; Pred. No. 11; Mismatches 11; Conservative 4; Indels 3; Gaps 1; Matches 4; Gap 1;

Qy 4 LIELTGWNIVNVSVILGVASHI 26
Db 9 LIALAFWVSVSV--GLSHV 28

RESULT 15

COME_HAEIN STANDARD: PRT; 173 AA.

ID COME_HAEIN ID P45036; DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cytochrome c-type biogenesis protein COME.
 GN COME OR H11093;
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / ATCC 51907;
 RX MEDLINE=9535630; PubMed=7542800;

RA Fretschmann-Riedl; Adams R.D.; White O.; Clayton R.A.; Kirkness E.F.; McKenney K.; Sutton G.; FitzHugh W.; Fields C.A.; Gocayne J.D.; Kerlavage A.R.; Bult C.J.; Tomb J.-F.; Dougherty B.A.; Merrick J.M.; Scott J.D.; Shirley R.; Liu L.-T.; Glodek A.; Kelley J.M.; Weidman J.F.; Phillips C.A.; Spriggs T.; Heidelberg J.; Cotton M.D.; Utterback T.R.; Hanna M.C.; Nguyen D.T.; Saudek D.M.; Brandon R.C.; Fine L.D.; Fritchman J.L.; Fuhrmann J.L.; Geoghegan N.S.M.; Gnevin C.L.; McDonald L.A.; Small K.V.; Fraser C.M.; Smith H.O.; Venter J.C.; random sequencing and assembly of Haemophilus influenzae

Query Match 24.6%; Score 51; DB 1; Length 458;
 Best Local Similarity 28.9%; Pred. No. 41; Mismatches 11; Conservative 9; Indels 18; Gaps 0; Matches 11; Gap 1;

Qy 4 LIELTGWNIVNVSVILGVASHI NYQPPEOSASVQ 41
Db 343 LIELTGWNIVNVSVILGVASHI NYQPPEOSASVQ 380

RT Rd. ";
 RL Science 269:496-512(1995).
 CC -!- FUNCTION: REQUIRED FOR THE BIOGENESIS OF C-TYPE CYTOCHROMES.
 CC POSSIBLE SUBUNIT OF A HEME LYASE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: MOSTLY PERIPLASMIC; ANCHORED IN THE INNER
 CC MEMBRANE (POSSIBLY).

-!- SIMILARITY: BELONGS TO THE CCME/CYCJ FAMILY.

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EMBL: B32789; AK022750.1; -
 DR TIGR; H11093; -
 DR InterPro; IPR004339; CcmE; 1.
 KW Cytochrome c-type biogenesis; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 9 29 POTENTIAL.
 DOMAIN 30 173 PEIPLASMIC (POTENTIAL);
 SEQUENCE 173 AA; 19149 MW; 0505AC6B99/09156 CRC64;
 Query Match 24.4%; Score 50.5; DB 1; Length 173;
 Best Local Similarity 40.5%; Pred. No. 18;
 Matches 15; Conservative 4; Mismatches 13; Indels 5; Gaps 2;
 OY 7 LITGWIVLVSVVILGVASHIDNQPPQQSASYQ--HK 41
 ||| :||| :||| ||| :||| ||| :||| ||| :||| ||| :|||
 Db 116 LQOPTVLTATEVL---AKHDENVVPPPELGKMQKVH 149

Search completed: February 6, 2003, 21:39:32
 Job time : 13 secs

GenCore version 5.1.3
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Om protein - protein search, using sw model

Run on:

February 6, 2003, 21:36:40 ; Search time 29 seconds

(without alignments)
291.308 Million cell updates/sec

Title: US-09-828-456-2

Perfect score: 207

Sequence: 1 MRNLIELTGTGIVLWVSVILLGVASHIDNYQPPEQSASVQHK 41

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21;*

SP_ARCHEA;*

SP_BACTERIA;*

SP_FUNGI;*

SP_HUMAN;*

SP_INVERTEBRATE;*

SP_MAMMAL;*

SP_MHC;*

SP_ORGANELLE;*

SP_PHAGE;*

SP_PLANT;*

SP_RODENT;*

SP_VIRUS;*

SP_VERTEBRATE;*

SP_UNCLASSIFIED;*

SP_RVIRUS;*

SP_BACTERIAPL;*

SP_ARCHEAP;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	96.6	41	16	Q8X361 escherichia
2	64	30.9	296	17	Q8TY57 methanopyru
3	63.5	30.7	254	2	Q9BY3 shewanella
4	58	28.0	332	16	Q98115 rhizobium l
5	58	28.0	344	10	Q8RWHB arabiopsis
6	57	27.5	440	2	Q52721 rhodobacter
7	57	27.5	460	2	Q9J906 rhodobacter
8	57	27.5	826	3	Q9uvb5 candida alb
9	56.5	27.3	309	13	Q8UWE8 tetradon n
10	56.5	27.3	318	13	Q8Qff3 tetrodion n
11	56	27.1	490	2	Q9XBM1 prausnitzella
12	55.5	26.8	623	16	Q8XN6 clostridium
13	55	26.6	219	16	Q97P36 streptococc
14	55	26.6	320	16	Q9CFA7 lactococcus
15	54.5	26.3	183	2	Q93JR2 rhabdoccus
16	54	26.1	374	17	Q97x02 sulfolobus

ALIGNMENTS

RESULT 1									
ID	SEQUENCE FROM N.A.	PRELIMINARY;	PRT;	41 AA.					
Q8X361	STRAIN=0157:H7 / RIMD 0509952;								
Q8X361;	MEDLINE=21156231; PubMed=11288796;								
	Hayashi T., Matano K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Onisubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakiawa C., Ogasawara N., Yasunaga T., Kubara S., Shiba T., Hattori M., Shingawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.", DNA Res. 8:11-12(2001)								
DR	EMBL; AP002558; BAB5756.1; -								
SQ	SEQUENCE 41 AA; 4600 MW; D384BB0167AA46B CRC64;								
RT	Query Match 96.6%; Score 200; DB 16; Length 41;								
RT	Best Local Similarity 95.1%; Pred. No. 7e-20;								
RL	Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;								
DR	QY 1 MRNLIELTGTGIVLWVSVILLGVASHIDNYQPPEQSASVQHK 41								
DB	1 MRNLIELTGTGIVLWVSVILLGVASHIDNYQPPEQSASVQHK 41								

RESULT 2

Q8TY57 PRELIMINARY; PRT; 296 AA.

Db	265	RLLLIGWLLIMLGVVLLVTSSSLIRHLP	293
RESULT	6		
ID	Q52721	PRELIMINARY;	PRT; 440 AA.
AC	Q52721;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DR	01-MAR-1996 (TREMBLrel. 01, last sequence update)		
DE	Sensor kinase.		
GN	RGB.		
OS	Rhodobacter capsulatus (Rhodopseudomonas capsulata).		
OC	Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;		
OX	NCBI_TaxID=1061;		
RN	[1]	SEQUENCE FROM N.A..	
RP	SEQUENCE FROM N.A..		
RX	STRAIN="SB1003";		
RX	MEDLINE="95059596; PubMed=8002581;		
RA	Mosley C.S., Suzuki J.Y., Bauer C.E.;		
RT	"Identification and molecular genetic characterization of a sensor kinase responsible for coordinately regulating light harvesting and reaction center gene expression in response to anaerobiosis [published erratum appears in J Bacteriol 1995 Jun;177(11):3359].";		
RL	J. Bacteriol. 176:7566-7573 (1994).		
CC	-1 SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE KINASES.		
DR	EMBL: L35179; AAC0144_1; -;		
DR	InterPro; IPR003594; ATPbind, ATPase.		
DR	InterPro; IPR003661; His_kinA.		
DR	InterPro; IPR004359; HIS_KIN_sig.		
DR	Pfam; PF02518; HATPase_c; 1.		
DR	SMART; SM0012; signal; 1.		
DR	SMART; SM00387; HATPase_c; 1.		
DR	SMART; SM00388; Hista; 1.		
KW	Kinase; Phosphorylation; Sensory transduction; Transferase.		
SQ	SEQUENCE 440 AA; 47410 MW; 8EE58A65C318C77 CRC64;		
Query Match	27.5%; Score 57; DB 2; Length 440;		
Best Local Similarity	40.9%; Pred. No. 18; Length 440;		
Matches	9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;		
QY	4 LIELTGWIVLWVSVLVLGVASH 25		
Db	146 MIEFGSWVAIVVIGVIFLGAYAH 167		
RESULT	7		
ID	Q9L906	PRELIMINARY;	PRT; 460 AA.
AC	Q9L906;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	sensor kinase.		
GN	RGB.		
OS	Rhodobacter capsulatus (Rhodopseudomonas capsulata).		
OC	Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;		
OC	Rhodobacter.		
OX	NCBI_TaxID=1061;		
RN	[1]	SEQUENCE FROM N.A..	
RP	SEQUENCE FROM N.A..		
RC	STRATENSBTO03;		
RX	MEDLINE="20100775; PubMed=10633119;		
RX	Chen W., Jager A., Klug G.;		
RT	"Correction of the DNA sequence of the regB gene of Rhodobacter capsulatus with implications for the membrane topology of the sensor kinase RegB.>";		
RT	J. Bacteriol. 182:818-820 (2000).		
GN	REGB.		
OS	Rhodobacter capsulatus (Rhodopseudomonas capsulata).		
OC	Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;		
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OC	Rhodobacter.		
OX	NCBI_TaxID=1061;		
RN	[1]	SEQUENCE FROM N.A..	
RP	SEQUENCE FROM N.A..		
RC	STRATENSBTO03;		
RX	MEDLINE="20		

OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;	RC	SISTRAIN-NRRL B-2295;											
OC	Tetraodontidae; Tetraodon.	RX	MEDLINE=21128526; PubMed=11207749;											
OX	NCBI_TAXID=9983;	RA	Smits T.H.M., Roethlisberger M., Witholt B., Van Beilen J.B.;											
RN	[1]	RT	"Molecular screening for alkane hydroxylase genes in Gram-negative and											
RA	Bestnot A.	RT	Gram-positive bacteria;"											
RT	* Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	RL	Eukary-Micrbiol 1:307-312(1999),											
RT	an amylase gene family. "	DR	EMBL; AU00957; CAB51024.2; -.											
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	DR	HSSP; P00268; 5RN.											
DR	EMBL; AU30823; GAC87122.1; -.	DR	InterPro; IPR001125; FA_desaturase.											
SQ	SEQUENCE FROM N.A.	DR	InterPro; IPR00039; Rubredoxin.											
OY	7 LTGKIV--LVNSVILL-----GVASHIDNKPPEQ 34	DR	InterPro; IPR001052; Rubredoxin.											
Db	231 LPGWILTTTLLVLSVLWICCATVATAVDQVTPAER 267	DR	Pfam; PF00487; FA_desaturase; 1.											
RESULT 10		DR	PF00301; Rubredoxin; 1.											
Q8QFS3	PRELIMINARY; PRT; 318 AA.	DR	PRINTS; PRO01163; RUBREDOXIN.											
ID Q8QFS3		DR	PRODOM; PD001610; Rubredoxin; 1.											
AC Q8QFS3;	DT 01-JUN-2002 (TREMBLrel. 21, Created)	DR	PROSITE; PS00202; RUBREDOXIN; 1.											
OC	Actinopterygii; Teleostei; Neofishes;	KW	Monooxygenase; Oxidoreductase.											
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	SQ	SEQUENCE 490 AA; 54700 MW; 83FAB425D05B5848 CRC64;											
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 309;											
DE	HOLCJC protein.	Db	Best local Similarity 40.5%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
GN	HOLCJC.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 309;											
OS	Tetraodon nigroviridis (Green puffer).	Db	Best local Similarity 36.8%; Pred. No. 28; Mismatches 6; MisMatches 14; Conservative 14; Indels 10; Gaps 8; Gaps 1;											
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 309;											
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neofishes;	Db	Best local Similarity 36.8%; Pred. No. 28; Mismatches 6; MisMatches 14; Conservative 14; Indels 10; Gaps 8; Gaps 1;											
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 309;											
OC	Tetraodontidae; Tetraodon.	Db	Best local Similarity 36.8%; Pred. No. 28; Mismatches 6; MisMatches 14; Conservative 14; Indels 10; Gaps 8; Gaps 1;											
OX	NCBI_TAXID=9983;	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 309;											
RN	[1]	Db	Best local Similarity 36.8%; Pred. No. 28; Mismatches 6; MisMatches 14; Conservative 14; Indels 10; Gaps 8; Gaps 1;											
RP	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 309;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 28; Mismatches 6; MisMatches 14; Conservative 14; Indels 10; Gaps 8; Gaps 1;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 309;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 28; Mismatches 6; MisMatches 14; Conservative 14; Indels 10; Gaps 8; Gaps 1;											
RA	Bonneau L.;	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 309;											
RT	Query Match 27.3%; Score 56.5; DB 13; Length 318;	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE 318 AA; 36409 MW; 42F2952DC7/005A CRC64;	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Query Match 27.3%; Score 56.5; DB 13; Length 318;	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RA	SEQUENCE FROM N.A.	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	"Analysis of 148 kb of genomic DNA of <i>Tetraodon nigroviridis</i> covering	Db	Best local Similarity 36.8%; Pred. No. 15; Mismatches 7; MisMatches 15; Conservative 15; Indels 9; Gaps 2;											
RT	an amylase gene family";	Qy	Query Match 27.3%; Score 56.5; DB 13; Length 318;											
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	Db	Best local Similarity 36.8%; Pred. No. 15; M											

ID	PRELIMINARY;	PRT;	219 AA.
AC	Q9P36;		
DT	01-OCT-2001 (TREMBREL, 18, Created)		
DT	01-OCT-2001 (TREMBREL, 18, Last sequence update)		
DT	01-DEC-2001 (TREMBREL, 19, Last annotation update)		
DE	Type IV prepilin peptidase, putative.		
GN	SPI808.		
OS	Streptococcus pneumoniae.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;		
OC	Streptococcaceae; Streptococcus.		
OX	NCBI_TAXID=113;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=TIGR4;		
RX	MEDLINE=21357209; PubMed=11463916;		
RA	Tettelin H., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Hirt D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapfle E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae"; Science 293:498-506(2001).		
DR	EMBL; AE007473; AACR75881.1; -.		
DR	TIGR; SPI808; -.		
DR	InterPro; IPR000045; Peptidase_C20.		
DR	Ptam; PF01478; Peptidase_C20; 1.		
DR	Complete proteome.		
DR	SEQUENCE 219 AA; 24843 MW; 9FB487E0994C90DF CRC64;		
QY	4 LIELTGWIVLVNVSVLVLGVASH 25		
Best Local Similarity 40.9%; Pred. No. 16; Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;			
Db	127 LIASSGNWNLVMSFLIGILAH 148		
RESULT 14			
AC	Q9CPA7; PRELIMINARY;	PRT;	320 AA.
DT	01-JUN-2001 (TREMBREL, 17, Created)		
DT	01-JUN-2002 (TREMBREL, 21, Last annotation update)		
DE	Hypothetical Protein yabP.		
GN	YOBF OR L11574.		
OC	Lactococcus lactis (subsp. lactis) (Streptococcus lactis). Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Lactococcus.		
OC	Streptococcaceae; Lactococcus.		
OS	"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis LIL403." Genome Res. 11:731-753(2001);		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=LIL403;		
RX	MEDLINE=21235186; PubMed=11337471;		
RA	Boletin A., Wincker P., Mauger S., Dujon B., Malarme K., Weissenbach J., Erlich S.D., Sorokin A.;"The complete genome sequence of the lactic acid bacterium Lactococcus		
RT	lactis ssp. lactis LIL403." Genom Res. 11:731-753(2001);		
RT	EMBL; AE006388; AAC05672.1; -.		
DR	InterPro; IPR003059; AB_hydrolase.		
DR	InterPro; IPR000724; Lipase.		
DR	InterPro; IPR003379; Ser_esters_site.		
DR	PRINTS; PR0011; ABHYDROLASE.		
DR	PROSITE; PS00120; LIPASE SER; UNKNOWN_1.		
DR	Hypothetical protein, Complete proteome.		
SQ	SEQUENCE 320 AA; 35901 MW; 2E06FBDB803461A CRC64;		
RESULT 15			
ID	Q93JR2	PRELIMINARY;	PRT;
AC	Q93JR2;		183 AA.
DT	01-DEC-2001 (TREMBREL, 19, Created)		
DT	01-JUN-2002 (TREMBREL, 21, Last annotation update)		
RA	Akane-1-monooxygenase (Fragment).		
DR	ALKB.		
DR	Rhodococcus fascians.		
DR	Bacterium; Firmicutes; Actinobacteridae; Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.		
OX	NCBI_TAXID=1828;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=L154 S;		
RA	Van Beilen J.B., Smits T.H.M., Balada S.B., Witholt B.;"Alkane hydroxylases in Gram-positive strains"; Submitted (DBEc-2000) to the EMBL/GenBank/DBJ databases.		
DR	InterPro; IPR001225; FA_desaturase.		
DR	Pfam; PF00487; FA_desaturase; 1.		
DR	PRINTS; PR01565; NEUROMEDINUR.		
KW	Monooxygenase.		
FT	NOL_TER	1	
FT	NOL_TER	183	183
SQ	SEQUENCE 183 AA; 21185 MW; 757649087E8C6D0 CRC64;		
QY	4 LIELTGWIVLVNVSVLVLGVASH 25		
Best Local Similarity 25.5%; Pred. No. 15; Matches 13; Conservative 13; Mismatches 12; Indels 13; Gaps 2;			
Db	106 LIAVFGWIVLPYLQIAAIATVLYEANVLEHYGLMTRRRPDGGRYAKPSR 156		
Search completed: February 6, 2003, 21:39:09			
Job time : 33 secs			